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CC103_HUMAN
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FLHB_AQUAE
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CIKA_RAT
CIKA_HUMAN
AG22_MOUSE
AG22_RAT
CIG4_HUMAN
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A. draggan,

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152 VVQRITVHVTRRPVLYFHIRW---

78 LGKFLSEHLVWLYGNYLKLKYLILSRHRKERREHVCEHCHSHGMGHDMNIEEKRIPAFLV 137

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Query Match
Best Local Similarity 27.0

12.7%;
27.0%;

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Score 222.5; DB 1; Pred. No. 5.3e-10; 50; Mismatches 63;

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EMBL; W34403; CAA64176.1; -
EMBL; U37254; AAC49168.1; -
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                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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SEQUENCE FROM N.A.
MEDLINE-96303826; PubMed-8723646;
Poid J.D., Lukas W., Shafaattan R.,
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Lesage F., Guillemare E., Fink M.,
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Eukaryota; Fungi; Ascomycota; Saccharomycetes;
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                                                                             use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Q10937;
Q1-NOV-1997
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      SEQUENCE
                                                    WORMPEP;
                                                               EMBL; U40959;
                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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TRANSMEM 72
TRANSMEM 138
TRANSMEM 171
TRANSMEM 204
TRANSMEM 247
TRANSMEM 302
TRANSMEM 380
TRANSMEM 436
CONFLICT 442
CONFLICT 512
SEQUENCE 691
                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                         Submitted (NOV-1995)
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                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                        Caenorhabditis elegans
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                                                                                                                                                                                  Favello
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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Pred. No. 2.7e
33; Mismatches
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                                                                                                  TRANSMEM SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                      jannaschii.";
Science 273:1058-1073(1996).
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                                                                                                                                                                                                                                                                                     the European
                                                                                                                                                                                                                                                                                                      between
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-1- SIMILARITY: STRONG, TO M.JANNASCHII MJ1357.
-1- SIMILARITY: TO EUKARYOTIC POTASSIUM CHANNEIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96337999; PubMed=8688087;
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LGFVTVSCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYK 246
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931069; P94716; P94717; P94723;

01-JUL-1993 (Rel. 26, Created)

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01-NOV-1997 (Rel. 35, Last annot
                                                                                                                                                                                             MEDLINE=97251357; PubMed=9097039;
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K
Aiba H., Rasai H., Kashimoto K., Kimura S., Kitakawa M.,
Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mo
Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio
Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
Yamamoto Y., Horluchi T.,
                                                                                                                                                                                                                                                                                                        SEQUENCE
STRAIN-K1
                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=K12 / MC1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A
Riley M., Collado-Vides J., Glasner J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.
STRAIN-K12, AND
                                                                                                                                                                      "A 570-kb DNA sequence of the Escherichia corresponding to the 28.0-40.1 min region
                                                                                                                                                                                                                                                                                                                                                Science
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MEDLINE=94224769; PI
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                                                                                                                                             ROLE IN THE DEFENSE
                                                                                                                               INTEGRAL
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                                                                                                                                                                                                                                                                                                                                                            Escherichia
                                                                                                                               MEMBRANE
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., Rode C.K., Mayhew
, Goeden M.A., Rose D
                                                                                                                                                                                                                                                              Inada T., Isono K.,
S., Kitakawa M.,
                                                                                                                                                                    coli K-12 genom
on the linkage
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                                                                                                                                             AGAINST
                                                                                                                                                                                                                                                                                                                                                            coli
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yhew G.F.,
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                                                            a collaboration -
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RESULT 6

Y139_METJA

ID Y139_METJA

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DT 01-NOV-1997

DT 01-NOV-1997
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TRANSMEM 64
TRANSMEM 87
TRANSMEM 111
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TRANSMEM 141
TRANSMEM 200
VARIANT 5
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BL; U24195; AAB60079.1;
BL; U24196; AAB60087.1;
BL; U24197; AAB60087.1;
BL; U24198; AAB60095.1;
BL; U24198; AAB60103.1;
BL; U24200; AAB60119.1;
BL; U24201; AAB60119.1;
BL; U24202; AAB60119.1;
BL; U24203; AAB60119.1;
BL; U24204; AAB60119.1;
BL; U24204; AAB60119.1;
BL; U24205; AAB60119.1;
BL; U24206; AAB60119.1;
BL; U2
                                                                                                                                     DVKTVLAVSDSKNLNKIKMVHPD-----IILSPQLFGSEI 372
                                                                                                                                                                                                                                                                                                                                    TVGYGDIVPVSESARLFTI------SVIISGITVFATSMTSIFGPLIRGGFN
                                                                                                                                                                                                                                                                                                                                                                                                                                   LKRRFLEEHECLSEQQLEQFLG--RVLEASNYGVSVLSNASGNWNWDFTSALFFASTVLS 116
                                                                                                                                                                                                   -----RLGDNADVIPGDSNDSSV--LKKAGIDRCRAILALSDNDADNAFVVLSAKDMSS
                                                                                                                                                                                                                                     ISLSTIGLG----DYVPGEGYNQKFRELYKIGI-TCYLLLGLI------AMLVV-----
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                                                                                                                                                                                                                                                                                                    KQVVAIVHAVLLGFVTVSCFFFIPA------AVFSVLEDDWNFLESFYFCF
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(Rel. 35, Created)
(Rel. 35, Last sequence
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                                                   STANDARD;
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22.5%;
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A -> T (IN STRAINS ECOR 52 AND ECOR 60

N -> K (IN STRAINS ECOR 4).

L -> O (IN STRAINS ECOR 4).

L -> O (IN STRAINS ECOR 4, ECOR 16, EC

28, ECOR 31, ECOR 37, ECOR 46, ECOR 52, ECOR 60 AND ECOR 71).

E -> K (IN STRAIN ECOR 46).

S -> U (IN STRAIN ECOR 46).

S -> U (IN STRAIN ECOR 46).

S -> U (IN STRAIN ECOR 46).
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Pred. No. 0.
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Query Match
Best Local
                                                                       _BACSU STANDARD; PRT; 393 AA P39141; 032288; Ol-FEB-1995 (Rel. 31, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 01-CCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
SEQUENCE
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MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute. There a
use by non-profit institutions as long as i
modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U67471; AAB98122.1; TIGR; MJ0139; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
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    Bacteria;
                                                               PYRIMIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jannaschii.";
Science 273:1058-1073(1996).
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                       Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanococcus jannaschii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 DFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTR 162
                                                                                                                                                                                                                                                                     ESGVNPAINNEFDAFYFTTISITTVGYGDITP----KTDAGKLIIIFSVLFFISGLITSL
                                                                                                                                                                                                                                                                                                                                                                                      EDDW-----NFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLLGLIAML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
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Firmicutes;
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11 33
72 9;
126 14(
157 17)
182 20
209 AA; 2
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21.7%;
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92
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  Bacillus/Clostridium group;
                                                               TRANSPORT
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Pred.
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                                                               PROTEIN
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No. 0.
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Query Match
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Matches 56
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CONFLICT
SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE SLC28A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-168 / BGSC1A1;
MEDLINE-9702144; PubMed-8867804;
Yoshida K.-I., Fujimyra M., Yanai N., Fuji
"Cloning and sequencing of a 23-kb region
genome between the iol and hut operons.";
                                                                                                                                                                                                                                                                             TRANSMEM TRANSMEM
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EMBL; D45912; BAA08338.1;
EMBL; Z99124; CAB15977.1;
SUBTILIST; BG10984; NUPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saxild H.H., Andersen L.N., Hammer K.; "Dra-nupC-pdp operon of Bacillus subtilis: nucleotide sequence, induction by deoxyribonucleosides, and transcriptional regulation the deoR-encoded DeoR repressor protein.";

J. Bacteriol. 178:424-434(1996).
                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO; IPR002668; -.
PFAM; PF01773; Nucleoside_tra2;
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                                                                                                                                                                                                                                                                                                                                                                                          Fransport;
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 194
                         292
                                               140
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                                                                                                                  CFFFIPAAVFSVLEDDWNFLESF--
                       VGIPWNEAVNAGSIMATKMVSNEFVAMTSLTQNGFH----FSGRTTAIVSVFLVSFANFS
                                               IGIPFT---
                                                                     VVVAAMLIGEVAIIALINGIEN-----AVEGISEQGILGY---
                                                                                             RVLEASNYG-VSVLSNASGNWNWDFTSALFFASTVLSTTGY(;HTVPLSDGGKAFCIIYSV
                                                                                                                                                                     1 Similarity
56; Conserv
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                                                                                                                                                                                                                Conservative
                                             LLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTVS
                                                                                                                                                                               5.7%;
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                                                                                                                                                                      32;
                                                                                                                                                                   Score 100.5;
Pred. No. 1;
32; Mismatches
                                                                                                                                                                                                                                       POTENTIAL.

F -> L (IN
SI -> RL (I
                                                                                                                                                                                                                                                                                         POTENTIAL.
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I -> RL (IN REF. 1).
-> V (IN REF. 1).
C28677B5D30AE0A( CRC64;
 -YFCFISLST:[GL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujita Y.;
gion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.
                                                                                                                                                                                          DB 1.;
                                                                                                                                                                     ; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus subtilis
                                                                                                                                                                                         Length
                                                                                                                                                                     Indels
                                                                     -----VFAPFAFL
                                                                                                                                                                                          . 393;
                                                                                                                                                                   47;
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                                                                                                                                                                  Gaps
                       347
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HLAEKTAKRTSYSRKEVLSYIFHHPALWVMMLLTMLTQTGNFSIQPLLALYVNELHGPVN 202

SOFFI

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RESULT 8
YUXJ_BACSU
ID YUXJ_BACSU
AC P40760;
                                                                                                              Matches
                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                       Hypothetical TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oudega B., Koningsteijn G., Rodrigues L., Hilbert H., Duesterhoeft A., Pohl T.M., We "Analysis of the Bacillus subtilis genomosequence of a 62 kb region be" (pai).":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995
15-JUL-1998
15-DEC-1998
                                                                                                                                                                                   TRANSMEM
SEQUENCE
                                                                                                                                                                                                                               TRANSMEM
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microbiology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein 4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Popham D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95050302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF
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                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, nucleotide sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348
143
                         55
                                                     83
                                                                                                                            Local
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                                                                                  ω
                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content ified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: INTEGRAL MEMBI SIMILARITY: STRONG, TO E.COLI YCEE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSLOCASE FAMILY.
                                                                                  QSLAGSSCVRLVERHRSAWCFGFLVLGYL-----LYLVFGAVVFSSVELPYEDLLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGIIAGAVKGLNEKQGNVVARFGLKLLYGATLVSFLSAAIVGL
                                                     KSSAGKTLGTLQMGQVSGSLFGPLLGGMLADRFGFTYTFFITSFVIFSSVLLVLFGVKEK 142
                                                                                                                                                                                                                                                                                                                             Z93933; CAB07914.1; -.
Z99120; CAB15137.1; -.
U11882; AAA64942.1; -.
                         EL--RKLKRRFLEEHECLS-----EQQLEQFLGRVLEASNYGVSVLSNASGNWNWDFTS 106
                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Firmicutes;
                                                                                                                                                                                              protein;
39 59
61 8
92 11
119 13
159 17
201 22
236 29
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(Rel.)
(Rel.)
(Rel.)
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                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Setlow P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143:2769-2774(1997).
                                                                                                                                                                                     ΑA;
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39105
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112
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Last seq
                                                                                                                                                                                                                                                                                   Transmembrane.
9 POTENTIAL.
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us group; Bacillus.
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Last annotation update)
PROTEIN IN KAPD-PBPD IN
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D E.COLI YCEE. SOME, TO THE
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                          Score 97.5;
Pred. No. 1
                                                                                                                                                                                   POTENTIAL.
31758C0122231311 CRC64;
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                                                                                                              Mismatches
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genome: cloning and
275 degrees / ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356
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                                                                                                             119;
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                                                                                                                                        Length 356;
                                                                                                              Indels
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E DRUG RESIS
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MBL outstation -
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                                                                                                             Gaps
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RESULT
CIKB_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIKE_RAT STANDARD; PRT; 802 AA. Q63099; Q63099; Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.2
                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                     PRINTS;
                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuron
                                                                                                        EMBL; M77482;
                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through
                                                   PFAM; PF00520; ion_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecular cloning and characterization."; Neuron 8:473-481(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92198655; PubMed=1550672;
Hwang P.M., Glatt C.E., Bredt D.S., Yellen G.,
"A novel K+ channel with unique localizations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                   Conic
                                                                   INTERPRO; IPR000636; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231
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                                                                                                                                                                                                                                                                                                                    EVERY THIRD POSITION.

DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL TO SPECIFIC SUBCE
                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: IN THE BRAIN, THE GREATEST DENSITY OCCU
THE OLFACTORY BULLS, FOLLOWED BY THE CEREBRAL CORTEX, HIPPOC
AND CEREBELLUM, IN PERIPHERAL TISSUES IT IS MOST PROMINENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THIS PRÓTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                           WHOLE TONGUE EPITHELIUM AND CIRCUMVALLATE PAPILLAE.

DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS:
                                                                                                                                                                                                                                                                           SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DEL. CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
                                                                                                                                                                                                                                                                                                             ACTIVITY AND/OR TARGETING COMPARTMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFIPAAVFSVLEDDWNFLESFYFCF
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                   channel;
                                     PR00169; KCHANNEL.
                                                                                                                                                                                                                        the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa;
                                                                                                      AAA40905.1; -.
Multigene family; Phosphorylation
               Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rodentia;
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                 Ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
                 transport;
                                                                                                                                                                                  There are no restrictions ong as its content is in
                                                                                                                                                                      Usage
                 Voltage-gated
                                                                                                                                                                                                                                                                                           TO THE DELAYED RECTIFIER
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mammalian brain:
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                                                                                                                                                                                                                                                                                                                             SUBCELLULAR
                   channel;
                                                                                                                                                                                                                                         a collaboration
                                                                                                                                                                        for
                                                                                                                                                                                                                         outstation
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RESULT 10
AG22_HUMAN STANDARD; PRT; 363 AA.
AC P50052; Q13016;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAY-2000 (Rel. 39, Last annotation update)
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Best Local
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DOMAIN
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DOMAIN
                    Chassagne C., Beatty B.G., Meloche S.: "Assignment of the human angiotensin II type 2 receptor gene to chromosome Xq22-qq2 by fluorescence in situ hybridization. Genomics 25:601-603(1995).
                                                                                                                                      "The
                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-LIVER;
MEDLINE=95251653; PubMed=7733925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                    TYPE-2 ANGIOTENSIN II RECEPTOR (AT2).
SEQUENCE FROM N.A
                                                                  MEDLINE-95309939; PubMed-7790004;
                                                                              TISSUE=PLACENTA;
                                                                                         SEQUENCE FROM N.A.
                                                                                                                Biochem.
                                                                                                                          angiotensin II receptor.
                                                                                                                                                  Martin
                                                                                                                                                                                                        Mammalia;
                                                                                                                                                                                                                                           AGTR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 LVERHRSAWCFGFLVLGYLLYLVFGAVVFSSVELP---YEDLLRQ--ELRKLKRRFLEEH
                                                                                                                                     sequence and genomic organization of the human
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                                                                                                                                                                                                                                                                                                                                                                                        FRELYKI -- GITCY -- LLLGLIAMLVVLETFCELHELKK 275
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                                                                                                                                                                                                                                                                                                                                                                                                               LLILFLAMGIMIFSSLVFFAEKDEDATKFTSIPASFWWATITMTTVGYGDIYPK-----
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                                                                                                                                                  M.M., Elton
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                                                                                                              Biophys.
                                                                                                                                                                                                        Eutheria;
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                                                                                                                Commun.
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EXTRACELLULAR (POTENTIAL).
SEGMENT S2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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POLY-SER.
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EMBL;
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Submitted (JUN-1995) to the EMBL/GenBank/DBJ distabases.

-i- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MAY HAVE A ROLE IN CELL
MORPHOGENESIS AND RELATED EVENTS IN GROWTH AND DEVELOPMENT.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-i- TISSUE SPECIFICITY: IN ADULT, HIGHLY EXPRESSED IN MYOMETRIUM WITH
LOWER LEVELS IN ADRENAL GLAND AND FALLOPIAN TUBE. VERY HIGHLY
EXPRESSED IN FETAL KIDNEY AND INTESTINE.

-i- SIMILARITY: BBLONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94242007; PubMed=8185599; Tsuzuki S., Ichiki T., Nakakubo H., Kitar Shirai H., Inagami T.; "Molecular cloning and expression of the "Molecular cloning and expression angiotensin II type 2 receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koike G., Horiuchi M., Yamada T., Szpirer C., Jacob H.J., I "Human type 2 angiotensin II receptor gene: Closed, mapped chromosome, and its mRNA is expressed in the human lung."; Biochem. Biophys. Res. Commun. 203:1842-1850(1994).
                GCRDB;
GCRDB;
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GCRDB;
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TISSUE-BLOOD;
Took) t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95091796; PubMed-7999093;
Martin M.M., Su B., Elton T.S.;
"Molecular cloning of the human angiotensin II type Biochem. Biophys. Res. Commun. 205:645-651(1994).
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MEDLINE-95236034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-1996) to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95236034; PubMed=7719706;
Lazard D., Briend-Sutren M.M., Villageois P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                          European
                                                                                                                                                        U20860; AAA85851.1;
L34579; AAA89990.1;
U10273; AAA61794.1;
U15592; AAA67762.1;
U16597; AAA67753.1;
U27478; AAA84900.1;
U27478; CAA61022.1;
P34996; IDDD.
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300034;
                GCR_1057;
GCR_1245;
GCR_1876;
GCR_2011;
GCR_2027;
GCR_2031;
GCR_2031;
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                                                                                                                                                                                                                                                                                                                                         and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
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pean Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Commun. 200:1449-1454(1934).
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loned, mapped
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P15387;
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CARBOHYD
CONFLICT
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DOMAIN
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INTERPRO; IPR000248; -.
INTERPRO; IPR000276; -.
PFAM; PF00001; 7tm_1; 1.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                        LTAVVQRITVHVTRRPVLYFHIRWGFSKQVVAIV-----HAVLLGFVTVSCFFFIPAAVF
                                                                                                                                                                                                           --FIIPLIFIATCYFGIRKHLLKTNSYGKNRITRDQVLKMAAAVVLAFIICWLPFHVLTF
                                                                                                                                                                                                                           WDFTSALFFAST-----VLSTTGYGHTVPLSDG----GKAFCIIYSVIGIPF-TLLF
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E; PS00237;
E; PS50262;
ein coupled
                                                                                                                                                                                                                                                                                                                                   Similarity
                             (Rel. 14, Created)
(Rel. 15, Last sequence update)
(Rel. 37, Last annotation update)
(Rel. 37, CHANNEL PROTEIN KV2.1
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G_PROTEIN_RECEP_F1_2;
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20.9%;
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EXTRACELLULAR
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EXTRACELLULAR (POTENTIAL).
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6 (POTENTIAL
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Craniata; Vert
Sciurognathi;
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Nature 340:642-645(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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EVERY THE TAIL MAY BE IMPORTANT IN MODULE THE TAIL MAY BE IMPORTANT IN MODULE THE CHANNEL
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DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NITTED (FEB-1990) to the EMBL/GenBank/DDBJ databases. FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSEI CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
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SIMILARITY: 1
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EXTRACELLULAR (POTENTIAL).
SEGMENT S2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SEGMENT S3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                         Score 95;
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y; Phosphorylation.
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61;

Conservative

55;

Mismatches 6

113;

Indels

52;

Gaps

14;

Similarity

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RESULT 12
CIKA_HUMAN
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Q14721;
15-JUL-1998
15-JUL-1998
15-JUL-1998
Glycoprotein; Multigene
DOMAIN 1 182
TRANSMEM 183 204
DOMAIN 205 224
                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                            the
                                                                                                                   EMBL; L02840; AAA36156.1; MIM; 600397; -.
                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ikeda S.R., Soler F.,
Submitted (JAN-1993) 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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DOMAIN: THE SEGMENT SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   da S.R., Soler F., Zuhlke R.D., Joho R.H., Lewis D.L., mitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
                                                                                                                                                                                                            ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
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                                                    channel;
                                                                              PF00520;
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                                                                PR00169;
                                                                                         IPR003091; -
                                                                                                       IPR000636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria;
                                                                                                                                                                                                                                                                  BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rel. 36, Last annotation update)
POTASSIUM CHANNEL PROTEIN KV2.1
                                                    Transmembrane;
                                                                              ion_trans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -VEAVCIAWFTMEYLLRFLSSPK----KWKFFKGPLNAIDLLAILPYYVTIF
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Primates;
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Last annotation updat
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          orane; Ion transport; Voltage-gated family; Phosphorylation. CYTOPLASMIC (POTENTIAL). SEGMENT S1 (POTENTIAL).
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IS PROBABLY THE VOLTAGE-SENSOR
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 EXTRACELLULAR
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Best Local S
Matches 61
                                                                                                                                                                                TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
TYPE-2 ANGIOTENSIN II RECEPTOR (AT2).
                               type 2 receptor. ;
Biochim. Biophys.
                                                         MEDLINE-94122216; PubMed-8292631; Ichiki T., Herold C.L., Kambayashi Y. "Cloning of the cDNA and the genomic
                                                                                                       SEQUENCE FROM N.A. STRAIN-BALB/C;
                                                                                                                                               Biochem.
                                                                                                                                                           Nakajima M., Mukoy "Cloning of cDNA a type 2 receptor.";
                                                                                                                                                                                                                                                             Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                              AG22_MOUSE P35374;
       SEQUENCE FROM N.A.
                                               "Cloning of the cDNA and type 2 receptor.";
                                                                                                                                                                                                                                                                                                          AGTR2.
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                                                                                                                                               Biophys. Res.
                                                                                                                                                                                                                                                   s (Mouse).
Metazoa; Chordata; C
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21.7%;
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analysis of
                                1189:247-250(1994)
                                                                                                                                                 Commun.
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EXTRACELLULAR (POTENTIAL).
SEGMENT S4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SEGMENT S5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
SEGMENT S6 (POTENTIAL).
SEGMENT S6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC. . .) (F
360DEB3E45731EDA CRC64;
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                            Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                           Bardhan
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thi; Muridae; Murinae; Mus
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T.,
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                                                                                                                                                                                                                                                               Mus
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     INTERPRO; IPRO00147; -.
INTERPRO; IPRO00248; -.
INTERPRO; IPRO00276; -.
PFAM; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR002341; ANGIOTENSINR.
PRINTS; PR00636; ANGIOTENSINR.
                                                        Phosphorylation.
DOMAIN
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EMBL; U11073;
PIR; JC2028;
                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                GCRDB; GCR_1010;
MGD; MGI:87966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCRDB; GCR_0890; -. GCRDB; GCR_1007; -.
                                               CARBOHYD
                                                                                                                                                                                                                                                                                         G-protein
                                                                                                                                                                                                                                                                                                     PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P34996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulated by transcription -2.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/C; TISSUE=LIVER; MEDLINE=95378283; PubMed=765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PTM: CARBOXYL-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96337434; PubMed=8726696;
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; U04828; AAC52128.1;
; U00766; AAC04933.1;
; L32840; AAB49539.1; i
; U11073; AAA82184.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCR_1010; -
                                                                                                                                                                                                                                                                                         coupled
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                                                                                                                                                                                                                                                                                         receptor;
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EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                          3 (POTENTIAL)
CYTOPLASMIC (1
4 (POTENTIAL)
                                                                                                                                                                                                                                                                                        Transmembrane; Glycoprotein;
                                                                                                                                                                                                                     CYTOPLASMIC
2 (POTENTIAL
                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL) 3 (POTENTIAL).
                                                                                                                                                                                                                                                             EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diau V.J.; "The growth-dependent expression of angiotensin II type 2 receptor is regulated by transcription factors interferon regulatory factor-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nahmias C., Cazaubon S.M., Sutren M., Masso Villageois P., Elbaz N., Strosberg A.D., "Molecular and functional characterization receptor in neuroblastoma NIE-115 cells.", Adv. Exp. Med. Biol. 396:167-173(1996).
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                            -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MAY HAVE A ROLE IN C MORPHOGENESIS AND RELATED EVERISIES IN GROWTH AND DEVELOPMENT:
-1- SUBSCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: ABUNDANT IN FETUS, LOWER LEVELS IN ADUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 270:20225-20230(1995)
                                                                                                                                                                                                                                                                          SER OR THE RESIDUES MAY BE PHOSPHORYLATED. FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mukoyama
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01-JUN-1994 (Rel. 29
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                                                    Dzau V.J., Jacob H.J.,

"Cloning, characterization, and
"Cloning, characterization, and
angiotensin II receptor gene.",
angiotension 26:998-1002(1995).
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Dzau V.J.;
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                                                                                                                                                                                                                                                                    Hamakubo T., Inagami T.;
"Molecular cloning of a novel angiotensin II receptor
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                    MEDLINE-96088876; PubMed-7490161;
Koike G., Winer E.S., Horiuchi M.,
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EMBL; D16840; BAA
EMBL; U01908; AAC
EMBL; U032663; AAA
EMBL; D43778; BAA
EMBL; D43778; BAA
EMBL; D43778; D3496; 1DD
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identification of its functional promoter region."; Biochim. Biophys. Acta 1262:155-158(1995).

i- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MAY HAVE A ROLE IN COMPRISED AND RELATED EVENTS IN GROWTH AND DEVELOPMENT.

i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

i- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN FETAL TISSUES, I BRAIN, SKIN WOUND AND ATRETIC OVARIAN FOLLICLES.

i- DEVELOPMENTAL STAGE: ABUNDANT IN WHOLE FETUS BUT DECREASES AFTER BIRTH. IN ADULTS IS HIGHLY EXPRESSED IN THE ADRENAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kobayashi S., Ohnishi J., Nibu Y
Ishii M., Murakami K., Miyazaki
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receptor; Transmembrane;
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PubMed=7599191;
Nibu Y.,
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                                                                                                                                                                                                                                                                                            VARIANTS DENA2 SER-276; CYS-285 AND SER-321.

MEDILINE=99299248; PubMed=10369879;

Coucke P.J., Van Hauwe P., Kelley P.M., Kunst H., Schatteman :

Van Velzen D., Meyers J., Ensink R.J., Verstreken M., Declau I

Marres H., Kastury K., Bhasin S., McGuirt W.T., Smith R.J.H.,

Cremers C.W.R.J., Van de Heyning P., Willems P.J., Smith S.D.
                                                                                                                                                                                                                              "Mutations in the KCNQ4 gene are responsible deafness in four DFNA2 families."; Hum. Mol. Genet. 8:1321-1328(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND VARIANT DENA2 SER-285.
MEDLINE-99148276; PubMed-10025409;
Kubisch C., Schroeder B.C., Friedrich T., Luet
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 HRSAWCFGFL---VLGYLLYL-VFGAVVF---SSVELPYEDLLRQELRKLKRRFLEEH--
                                                      OF THE HAIR CELL.

SUBGELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: EXPRESSED IN THE OUTER, BUT NOT THE INNE
SENSORY HAIR CELLS OF THE COCHLEA.

DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS
EVERY THIRD POSITION (BY SIMILARITY).

DISEASE: DEFECTS IN KCNQ4 ARE A CAUSE OF AUTOSOMAL DOMINANT
NONSYNDROMIC SENSORINEURAL DEAFNESS TYPE 2 (DFNA2).

SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECT
                                                                                                                                                                                                                    FUNCTION: MAY BE RESPONSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WDFTSALFFAST-----VLSTTGYGHTVPLSDG----GKAFCIIYSVIGIPF-TLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTAVVQRITVHVTRRPVLYFHIRWGFSKQVVAIV----HAVLLGFVTVSCFFFIPAAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --FIIPLIFIATCYFGIRKHLLKTNSYGKNRITRDQVLKMALAVVLAFIICWLPFHVLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLVWCMACLS--SLPTFYFRDVRTIEYLGVNACIMAFPPEKYAQWSAGIALMKNILG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDALTWMGIIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ECLSEQQLEQFLGRVLEASNY--------
                                            KQT SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -VNPFLYCEV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SCEVIAVIDLALPFATLLGF-TNSC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 94.5;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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 produced through a collaboration -
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                                                                                                                                                                                                                                                                                                                                                                                                                                         sensory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO; IPR000636;
INTERPRO; IPR003091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
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MIM; 600101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ionic channel; Transmembrane; Ion transport; Voltage-gated
                  257
                                                      257
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                                                                                                                                                            155
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                                                    YLAEKDANSDFSSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAG
                                                                                                                                                                                                                                                                                                       YEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNAS----GNWNWD
                                                                                                                                                                                                                                                                                                                                                                            AGSSC------VRLVERHRSAWCFGFLVLGYLLYLVFGAVVFSSVELP
                                                                                                                                                           RI-----TVHVTRR-----PVLYFHIRWGFSKQVVAIVHAVLLGF-VTVSCFFFI
                                                                                                                                                                                                FRFA--
                                                                                                                                                                                                                                  FTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTL-----LFLTAVVQ
                                                                                                                                                                                                                                                                     QE---HQEL----ANECL---LILEFVMIVVFGLEYIVRVWSAGCCCRYRGWQGR
                                                                                                                                                                                                                                                                                                                                          SGSACGQRSSAAHKRYRRLQNWVYNVLERPR-GWAFVYHV--FIFLLVFSCLVLSVLSTI
                                                                                                                         SMRFLQILRMVRMDRRGGTWKLLGSVVYAH----
                                                                                     PAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYK-IGITCYLL-LG
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AF105216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e family;
45
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132
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276
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9; KCHANNEL
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AAD14681.
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AAD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77091 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                5.4%;
21.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VAR_008726;
G -> C (IN DFNA2; LOSS OF |
SELECTIVITY OF THE PORE).
/FTId=VAR_008727.
G -> S (IN DFNA2).
G -> S (IN DFNA2).
G -> S (IN DFNA2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOINED
                  278
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 94;
Pred. No.
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POTENTIAL.
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/FTId=VAR_008728.
A58737BD845ElA3A CRC64;
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                                                                                                                         -SKELIT---AWYIGFLVLIFASFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFNA2).
                                                                                                                                                                                                                                                                                                                                                                                                                 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     695;
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Search completed: February 14, 2001, 03:43:05 Job time: 28254 sec